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Genome Announcement

Complete genome sequence of human pathogen *Kosakonia cowanii* type strain 888-76^T



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ABSTRACT

Kosakonia cowanii type strain 888-76^T is a human pathogen which was originally isolated from blood as NIH group 42. In this study, we report the complete genome sequence of *K. cowanii* 888-76^T. 888-76^T has 1 chromosome and 2 plasmids with a total genome size of 4,857,567 bp and C+G 56.15%. This genome sequence will not only help us to understand the virulence features of *K. cowanii* 888-76^T but also provide us the useful information for the study of evolution of *Kosakonia* genus.

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Kosakonia cowanii (formally *Enterobacter cowanii*) is a Gram-negative, motile, rod-shaped pathogen, which was originally isolated from blood as NIH group 42.^{1,2} Although the type strain was first isolated from patient, this species were also frequently isolated from plant, soil and infant formula.^{3,4} These results suggest the diversity of this species. Although *K. cowanii* becomes more and more important, the complete genome sequence of this species has still not been reported. In this case, the type strain of this species, *K. cowanii*

888-76^T was completely sequenced in this study. This genome sequence will not only help us to understand the virulence features of this species but also provide useful information for understanding the evolution of *Kosakonia* genus.

The culture of strain 888-76^T used to prepare genomic DNA for sequencing was a laboratory stock and grown on LB (Lysogeny Broth, BD, USA) at 37 °C with vigorous shaking. 2.5 mL of culture broth was used to isolate the genomic DNA by using Wizard Genomic DNA Purification Kit (Promega,

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Madison, WI, USA). The quality of purified genomic DNA was tested by using NanoDrop 2000 UV-vis spectrophotometer (Thermo Scientific, MA, USA). Sequencing was performed on the PacBio RS II sequencer. After read filtering and adapter trimming, the genome was first *de novo* assembled using HGAP assembly protocol. After this first round, PBJelly V14.1.14 was used to fill and reduce as many captured gaps as possible to produce upgraded draft genomes.⁵

Protein coding genes, tRNA and rRNA annotations was done by NCBI Prokaryotic Genome Annotation Pipeline.⁶ In addition, GO and COG programs were used to further functional analysis of all annotated ORFs.^{7,8} Specifically, the virulence genes and MDR genes were searched based on VFDB and ARGannot.^{9,10}

The genome of *K. cowanii* 888-76^T consists of one circular chromosome (4,647,241 bp, 56.2% G+C), and two circular plasmid, named as p888-76-1 (113,443 bp, 53.5% G+C) and p888-76-2 (96,883 bp, 56.2% G+C) respectively. A total of 4448 CDSs were predicted. Of these, 3347 could be assigned to a COG number. In addition, 107 RNAs including rRNA and tRNA were identified. Strikingly, after searching at ARGannot database, we found 23 genes were responsible for antibiotic resistance. Of these, 6 genes encode β -lactamase, which is a typical features in *Enterobacteriaceae* strains.¹¹ 262 genes were predicted to be virulence genes, suggesting the pathogenesis of this strain. In these, 9 genes are encoded for type III secretion system, 5 genes are related to type IV pilus biogenesis and 41 genes are flagellar associated genes. The genomic information of *K. cowanii* 888-76^T will be important to clarify the virulence and MDR mechanisms as well as for understanding the evolution history of *Kosakonia* genus.

The assembled contigs were deposited in DDBJ/ENA/GenBank and published in the accession number CP019445 (chromosome), CP019446 and CP019447 (Plasmid). The version described in this paper is the first version.

Conflicts of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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